

Gencore version 4.5  
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:09:13 ; Search time 299.73 Seconds

(without alignments)

16.815 Million cell updates/sec

Title: US-09-331-631a-3\_COPY\_74-116

Perfect score: 250

Sequence: 1 NQDPDQTDQQCQRRCRQEE... RQQYCQRCKEICEEEYY 43

Scoring table: BLOSUM62

GapOp 10.0 , GapExt 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : SPTREMBL\_15; \*

1: sp\_archea; \*  
 2: sp\_bacteria; \*  
 3: sp\_fungi; \*  
 4: sp\_human; \*  
 5: sp\_invertebrate; \*  
 6: sp\_mammal; \*  
 7: sp\_mhc; \*  
 8: sp\_organelle; \*  
 9: sp\_phage; \*  
 10: sp\_plant; \*  
 11: sp\_rabbit; \*  
 12: sp\_virus; \*  
 13: sp\_vertebrate; \*  
 14: sp\_unclassified; \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

RESULT 1  
 Q9SP14 PRELIMINARY; PRT; 666 AA.  
 ID Q9SP14; AC Q9SP14; DT 01-MAY-2000 (TRIMBBLrel. 13, Created)  
 DT 01-MAY-2000 (TRIMBBLrel. 13, Last sequence update)  
 DT 01-OCT-2000 (TRIMBBLrel. 15, Last annotation update)  
 DE VICILIN PRECURSOR.  
 GN AMP2.  
 OS Macadamia integrifolia (Macadamia nut).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.  
 OC NCBI\_TaxID=6093;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=NUT KERNEL;  
 RA Marcus J.P., Goultier K.C., Green J.I., Manners J.M.;  
 RT "A family of antimicrobial Peptides is produced by processing of a 7S  
 RL globulin protein in Macadamia integrifolia.";  
 DR EMBL; AF161884; AAD4245.1; -.  
 DR HSSP; P0253; 2HBL.  
 DR INTERPRO; IPR00113; -.  
 DR PFAM; PF00546; Seedstore\_7S; 1.  
 SQ SEQUENCE 666 AA; 78243 MW; 0ECA22F8710F8ATB CRC64;  
 Query Match 100.0%; score 250; DB 10; Length 666;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-23;  
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q9SP15 macadamia i  
 Q9SP15 macadamia i  
 Q9SP13 macadamia i  
 Q9SEW4 juglans reg  
 Q9SEW4 juglans reg  
 Q93384 theobroma c  
 P91419 caenorhabdi  
 Q9594 caenorhabdi  
 Q17400 caenorhabdi  
 Q17401 caenorhabdi  
 Q9zw13 cucurbita m  
 Q9919 caenorhabdi  
 Q19051 caenorhabdi  
 Q18118 caenorhabdi  
 Q9n41 caenorhabdi  
 Q16501 caenorhabdi  
 Q16501 caenorhabdi  
 Q16502 caenorhabdi  
 Q16511 caenorhabdi  
 Q9na38 caenorhabdi

RESULT 2  
 Q9SP15 PRELIMINARY; PRT; 666 AA.

Q9SP15 AC Q9SP15; DT 01-MAY-2000 (TRIMBBLrel. 13, Created)

Db 74 NQDPDQTDQQCQRRCRQEE... RQQYCQRCKEICEEEYY 116

Q9SP14 macadamia i  
 Q9SP15 macadamia i  
 Q9SP13 macadamia i  
 Q9SEW4 juglans reg  
 Q93384 theobroma c  
 P91419 caenorhabdi  
 Q9594 caenorhabdi  
 Q17400 caenorhabdi  
 Q17401 caenorhabdi  
 Q9zw13 cucurbita m  
 Q9919 caenorhabdi  
 Q19051 caenorhabdi  
 Q18118 caenorhabdi  
 Q9n41 caenorhabdi  
 Q16501 caenorhabdi  
 Q16501 caenorhabdi  
 Q16502 caenorhabdi  
 Q16511 caenorhabdi  
 Q9na38 caenorhabdi

Q9SP15 PRELIMINARY; PRT; 666 AA.

Q9SP15 AC Q9SP15; DT 01-MAY-2000 (TRIMBBLrel. 13, Last sequence update)

Db 74 NQDPDQTDQQCQRRCRQEE... RQQYCQRCKEICEEEYY 116

DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE VICILIN PRECURSOR.  
 DE AMP2.  
 OS Macadamia integrifolia (Macadamia nut).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.  
 OC NCBI\_TaxID=60598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=NUT KERNEL;  
 RA Marcus J.P., Goulet K.C., Green J.L., Manners J.M.;  
 RT A family of antimicrobial peptides is produced by processing of a 7S  
 RT globulin protein in Macadamia integrifolia kernels.;  
 RL Plant J. 0:0-0(1999);  
 DR EMBL: AF01883; AAD4244.1; -.  
 DR INTERPRO: P0253; 2PHL.  
 DR PFAM: PF00546; Seedstore\_7s; 1.  
 SQ SEQUENCE 666 AA; 78217 MW; C752B884B2DF0224 CRC64;

Query Match 96.8%; Score 242; DB 10; Length 666;  
 Best Local Similarity 95.3%; Pred. No. 3.8e-22; Mismatches 0; Indels 0; Gaps 0;  
 Matches 41; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NQDDPQTDCQCRCRQDQESGPROQQYCORRCKEICEEEFY 43  
 Db 74 NOEDIPTECQCQRCRQDQESGPROQQYCORRCKBICEEEFY 116

RESULT 3  
 Q9SPJ3 PRELIMINARY; PRT; 625 AA.  
 ID Q9SPJ3; AC Q9SPJ3;  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE VICILIN PRECURSOR (FRAGMENT).  
 GN AMP2.  
 OS Macadamia integrifolia (Macadamia nut).  
 OC Eukaryota; Viridiplantae; Embryophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.  
 RN NCBI\_TaxID=60598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=NUT KERNEL;  
 RA Marcus J.P., Goulet K.C., Green J.L., Manners J.M.;  
 RT "A family of antimicrobial peptides is produced by processing of a 7S  
 RT globulin protein in Macadamia integrifolia.";  
 RL Plant J. 0:0-0(1999);  
 DR EMBL: AF01885; AAD54246.1; -.  
 DR HSSP: P0253; 2PHL.  
 DR INTERPRO: IPR001113; -.  
 DR PFAM: PF00546; Seedstore\_7s; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 625 AA; 73586 MW; 415808AB9D370296 CRC64;

Query Match 94.0%; Score 235; DB 10; Length 625;  
 Best Local Similarity 93.0%; Pred. No. 2.6e-21; Mismatches 1; Indels 0; Gaps 0;  
 Matches 40; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NQDPDQPTDCQCRCRQDQESGPROQQYCORRCKEICEEEFY 43  
 Db 33 NOEDIPTECQCQRCRQDQESGPROQQYCORRCKBICEEEFY 75

RESULT 4  
 Q9SEW4 PRELIMINARY; PRT; 593 AA.  
 ID Q9SEW4;  
 AC Q9SEW4;  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update);  
 DR 01-MAY-2000 (TREMBLrel. 13, Last sequence update);

Query Match 44.8%; Score 112; DB 10; Length 525;  
 Best Local Similarity 47.5%; Pred. No. 2.7e-06; Mismatches 11; Indels 0; Gaps 0;  
 Matches 19; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Qy 2 ODDPQPTDCQCRCRQDQESGPROQQYCORRCKEICEEEFY 41  
 Sq SEQUENCE 525 AA; 60798 MW; 19114CD5C248905D CRC64;

Db	78	EEELQRQYQQCQGRCQEQQQGOREQQCQRKCWEOYKOE	117	RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RESULT	6			CC -1- SIMILARITY: BELONGS TO FAMILY UPF.
ID	P91419	PRELIMINARY;	PRT;	411 AA.
AC	P91419			EMBL: U51997; AC48159.1; -.
DT	01-MAY-1997	(TREMBLrel. 03, Created)		DR WORMPEP: F19G12.7; CS07090.
DT	01-MAY-1997	(TREMBLrel. 03, Last sequence update)		
DT	01-NOV-1998	(TREMBLrel. 08, Last annotation update)		
DE	CODED FOR BY C. ELEGANS CDNA YK115A6.5.			
GN	T01D1.6.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;			
OC	Rhabditidae; Peioderinae; Caenorhabditis.			
OX	NCBI_TAXID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BRISTOL N2;			
RX	MEDLINE=9450718; PubMed=7906398;			
RA	Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,			
RA	Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,			
RA	Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,			
RA	Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,			
RA	Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,			
RA	Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,			
RA	Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showman R.,			
RA	Simlton N., Smith A., Sonnenburg E., Staden R., Sulston J.,			
RA	Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,			
RA	Watson A., Weinstock L., Wilkinson-Sproat J., Wohlgemuth P.,			
RT	*2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans ";			
RL	Nature 368:32-38(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BRISTOL N2;			
RA	Bradshaw H., Wohlgemuth P.;			
RL	Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BRISTOL N2;			
RA	Waterson R.;			
RL	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.			
SQ	SEQUENCE 411 AA; 44675 MW; 599DAC9DFAB1382 CRC64;			
RESULT	7			RESULT 8
ID	Q19594	PRELIMINARY;	PRT;	425 AA.
AC	Q19594			CC -1- SIMILARITY: BELONGS TO FAMILY UPF.
DT	01-JUN-1998	(TREMBLrel. 06, Created)		DR EMBL: Z71177; CA94867.1; -.
DT	01-JUN-1998	(TREMBLrel. 06, Last sequence update)		
DT	01-OCT-2000	(TREMBLrel. 15, Last annotation update)		
DE	HYPOTHETICAL 62.4 KDA PROTEIN F19G12.7 IN CHROMOSOME X PRECURSOR.			
GN	F19G12.7.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoidea; Rhabditida; Rhabditoidea;			
OC	Rhabditidae; Peioderinae; Caenorhabditis.			
OX	NCBI_TAXID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BRISTOL N2;			
RA	Nhan M., Le T.T.,			
RESULT	7			RESULT 9
ID	Q17401	PRELIMINARY;	PRT;	600 AA.
AC	Q17401			CC -1- SIMILARITY: BELONGS TO FAMILY UPF.
DT	01-JAN-1999	(TREMBLrel. 09, Created)		DR EMBL: U51997; AC48159.1; -.
DT	01-JAN-1999	(TREMBLrel. 09, Last sequence update)		
DT	01-JUN-2000	(TREMBLrel. 14, Last annotation update)		
DE	HYPOTHETICAL 67.7 KDA PROTEIN AC3.4 IN CHROMOSOME V.			
GN	AC3.4.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoidea; Rhabditida; Rhabditoidea;			
OC	Rhabditidae; Peioderinae; Caenorhabditis.			
OX	NCBI_TAXID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BRISTOL N2;			
RA	McMurray A.;			
RA	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BRISTOL N2;			
RA	McMurray A.;			
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: BELONGS TO FAMILY UPF.			
DR	EMBL: Z71177; CA94867.1; -.			
DR	WORMPEP; AC3.3; CE05133.			
KW	HYPOTHETICAL protein; Signal.			
FT	SIGNAL_	1	POTENTIAL.	
FT	CHAIN	22	425	HYPOTHETICAL PROTEIN AC3.3.
SEQUENCE	425 AA; 45922 MW; 951352A2AFF7E56C CRC64;			
RESULT	9			RESULT 10
ID	Q17401	PRELIMINARY;	PRT;	600 AA.
AC	Q17401			CC -1- SIMILARITY: BELONGS TO FAMILY UPF.
DT	01-JAN-1999	(TREMBLrel. 09, Created)		DR EMBL: U51997; AC48159.1; -.
DT	01-JAN-1999	(TREMBLrel. 09, Last sequence update)		
DT	01-JUN-2000	(TREMBLrel. 14, Last annotation update)		
DE	HYPOTHETICAL 67.7 KDA PROTEIN AC3.4 IN CHROMOSOME V.			
GN	AC3.4.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoidea; Rhabditida; Rhabditoidea;			
OC	Rhabditidae; Peioderinae; Caenorhabditis.			
OX	NCBI_TAXID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BRISTOL N2;			
RA	McMurray A.;			
RA	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			

CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
EMBL	Z71177; CAA98686.1; -.
DR	WORMPEP; AC3.4; CE05134.
DR	INTERPRO; IPRO011594; -.
DR	PFAM; PF01529; zf-DHHC; 1.
DR	PRODOM; PD003041; -; 1.
FT	KW HYPOTHETICAL protein; transmembrane.
FT	TRANSMEM 309 329 POTENTIAL.
FT	TRANSMEM 447 467 POTENTIAL.
FT	TRANSMEM 490 510 POTENTIAL.
FT	DOMAIN 6 287 GLN-RICH.
SQ	SEQUENCE 600 AA; 67740 MW; 504A5CE1BA72091B CRC64;
RESULT	10
Q9ZWL3	Query Match 31.0%; Score 77.5; DB 5; Length 600; Best Local Similarity 40.0%; Pred. No. 0.051; Mismatches 18; Conservative 9; Indels 11; Gaps 4; Matches 18; Last sequence update
Q9ZWL3	ID 09ZWL3; PRELIMINARY; PRT; 810 AA.
AC	09ZWL3; (TREMBLrel. 10, Last sequence update)
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE	PV100.
OS	Cucurbita maxima (Pumpkin) (Winter squash).
OC	Eukaryota; Viridiplantae; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
OX	NCBI_TaxID=3611;
[1]	SEQUENCE FROM N.A.
RP	STRAIN=KUROKAWA_AMAKURI_NANKIN; TISSUE=COTYLEDON; MEDLINE=9910919; PubMed=9891029;
RA	Yamada K., Shimada T., Kondo M., Nishimura M., Hara-Nishimura I.; "Multiple functional proteins are produced by cleaving Asn-Gln bonds of a single precursor by vacuolar processing enzyme."; J. Biol. Chem. 274:2563-2570(1999).
DR	EMBL; AB019195; BAA34056.1; -.
DR	HSRP; P02853; 2PHL.
DR	INTERPRO; IPR001113; -.
PFAM; PF00546; Seedstore_7s; 1.	PFAM; PF00546; Seedstore_7s; 1.
PRODOM; PD081059; -; 1.	PRODOM; PD081059; -; 1.
SEQUENCE	810 AA; 97314 MW; A829A3F7542666AB CRC64;
SQ	SEQUENCE 810 AA; 97314 MW; A829A3F7542666AB CRC64;
Query	Match 30.8%; Score 77; DB 10; Length 810; Best Local Similarity 34.2%; Pred. No. 0.076; Mismatches 13; Conservative 10; Indels 15; Gaps 0; Matches 13; Last sequence update
Q9Y	5 P071CQOCQCORRCRQOESGPRQQQCQRCRKEICEREEE 42
Q9Y	1: : : 1: 11: - 1: 11: 1: 1: 1: 1: 1: 1: 1: 11
Db	74 PRAEYEVCRILCQVAERGVQEYQEEERLREQ 111
RESULT	11
Q9919	Query Match 29.2%; Score 73; DB 5; Length 111; Best Local Similarity 41.9%; Pred. No. 0.047; Mismatches 13; Conservative 13; Last sequence update
Q9919	ID 09919; PRELIMINARY; PRT; 242 AA.
AC	09919; (TREMBLrel. 06, Last sequence update)
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT	01-JUN-1998 (TREMBLrel. 06, Last annotation update)
DE	HYPOTHETICAL 26.2 KDA PROTEIN F31A3.1 IN CHROMOSOME X.
GN	F31A3.1.
OS	Cenorhabditis elegans.
OC	Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidae; Rhabditidae; Pelerodinae; Caenorhabditis.
OX	NCBI_TaxID=6239;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	McMurray A.; Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RL	[2]
RP	SEQUENCE FROM N.A.
RA	MEDLINE=94150718; PubMed=7906398;
RA	Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A., Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Lalister N., Latreille P., Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showman R., Smalton N., Smith A., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sprout J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.;" Nature 368:32-38(1994).
RA	DR EMBL; 266496; CAA01281.1; -.
RL	Nature 368:32-38(1994).
DR	EMBL; 266496; CAA01281.1; -.
SQ	SEQUENCE 111 AA; 11681 MW; AFR595F0DA154F33 CRC64;
RESULT	12
Q9054	Query Match 29.4%; Score 73.5; DB 5; Length 242; Best Local Similarity 33.3%; Pred. No. 0.076; Mismatches 17; Conservative 17; Last sequence update
Q9054	ID 09054; PRELIMINARY; PRT; 111 AA.
AC	09054; (TREMBLrel. 01, Last sequence update)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT	01-JAN-1999 (TREMBLrel. 09, Last annotation update)
DE	E0AD5.4 PROTEIN.
GN	E0AD5.4.
OS	Caenorhabditis elegans.
OC	Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidae; Rhabditidae; Pelerodinae; Caenorhabditis.
OX	NCBI_TaxID=6239;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	McMurray A.; Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RL	[2]
RP	SEQUENCE FROM N.A.
RA	MEDLINE=94150718; PubMed=7906398;
RA	Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A., Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Lalister N., Latreille P., Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showman R., Smalton N., Smith A., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sprout J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.;" Nature 368:32-38(1994).
RA	DR EMBL; 266496; CAA01281.1; -.
RL	Nature 368:32-38(1994).
DR	EMBL; 266496; CAA01281.1; -.
SQ	SEQUENCE 111 AA; 11681 MW; AFR595F0DA154F33 CRC64;
RESULT	13
Q9118	Query Match 29.2%; Score 73; DB 5; Length 111; Best Local Similarity 41.9%; Pred. No. 0.047; Mismatches 13; Conservative 13; Last sequence update
Q9118	ID 09118; PRELIMINARY; PRT; 330 AA.

AC 018118;  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)  
 DE T23FL6. PROTEIN.  
 GN OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderrinae; Caenorhabditis.  
 OX NCBI\_TAXID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wilkinson J.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Riffen L., Roopra A., Saunders D., Showkeen R.,  
 RA Shalldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,  
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 RA Watson A., Weinstock L., Wilkinson-Sprott J., Wohldman P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 elegans." Nature 368:32-38(1994).  
 DR EMBL; 281129; CAB03405:1; -.  
 SQ SEQUENCE 330 AA; 36605 MW; F043B1A90D3A8FE9 CRC64;

Query Match 28.8%; Score 72; DB 5; Length 339;  
 Best Local Similarity 29.5%; Pred. No. 0.15; Matches 13; Conservative 10; Mismatches 9; Indels 12; Gaps 2;

QY 7 TPDQQCQCRRCRQO-----ESGPQQQ--YCPORCKEICE 38  
 DB 230 TNCQQCQNSQNSNTQTTIYQASQTSQVPCQOCQQCQ 273

RESULT 14

Q9N4R1 Q9N4R1 PRELIMINARY; PRT; 339 AA.  
 ID Q9N4R1; STRAIN=BRISTOL N2;  
 AC 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE HYPOTHETICAL PROTEIN Y5H2A.C.  
 GN Y5H2A.C.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;  
 OC NCBI\_TAXID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=BRISTOL N2;  
 MEDLINE=99069613; PubMed=9851916;

None;  
 "Genome sequence of the nematode *C. elegans*: a platform for investigating biology. The *C. elegans* Sequencing Consortium." Science 282:2012-2018(1998).  
 [2]

RP SEQUENCE FROM N.A.  
 RA STRAIN=BRISTOL N2;  
 RA Waterston R.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AC006809; AACF5626.1; -.  
 SQ SEQUENCE 339 AA; 36218 MW; 40233423237C432D CRC64;

Query Match 28.8%; Score 72; DB 5; Length 339;  
 Best Local Similarity 32.5%; Pred. No. 0.23; Matches 13; Conservative 10; Mismatches 11; Indels 6; Gaps 2;

QY 6 QTDQQCQCRRC-----RQOBSPGPROQYCRRCICEE 39  
 DB 194 QDQCCPQCCQCCQSSQVQQQDNOCEPAGNQCDICQ 233

Search completed: March 1, 2001, 16:09:14  
 Job time: 1558 sec

